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Figure 1 ·

```
                        forward
GNSQ_1754  gaggta atg aat gtc att gtt tta cag ttt att ctt ctt gtg ttt ctt ctt   51
p1754             Met Asn Val Ile Val Leu Gln Phe Ile Leu Leu Val Phe Leu Leu    15
                  §               §   §           §   §   §   §       §   §

GNSQ_1754         gtg aag ata tat aag cat gca gac aca cta ttt tat ata tat ata   96
p1754             Val Lys Ile Tyr Lys His Ala Asp Thr Leu Phe Tyr Ile Tyr Ile    30
                  §

GNSQ_1754         cct ata tat gta tgt atg tgt ata cac agt tat gca ctg tat aac   141
p1754             Pro Ile Tyr Val Cys Met Cys Ile His Ser Tyr Ala Leu Tyr Asn    45
                                  §       §

GNSQ_1754         agt att ttg gtc agt gat gga ctg cgt atg cta agg tgt tcc cat   186
p1754             Ser Ile Leu Val Ser Asp Gly Leu Arg Met Leu Arg Cys Ser His    60
                                                              §

GNSQ_1754         aag att ata ata agt act ttg act ata act ttt cta tgt tta cat   231
p1754             Lys Ile Ile Ile Ser Thr Leu Thr Ile Thr Phe Leu Cys Leu His    75
                                                          §

GNSQ_1754         gca gaa ata ctt act aat ggg tta cag ttg cct aca gta ttc agt   276
p1754             Ala Glu Ile Leu Thr Asn Gly Leu Gln Leu Pro Thr Val Phe Ser    90

                        reverse
GNSQ_1754         aca cca gca tgc tgt aca ggt tgg tag                            303
p1754             Thr Pro Ala Cys Cys Thr Gly Trp STOP                           98
                              §
```

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Figure 2

```
                           forward
GNSQ_0711  agcatt  atg gtt att cca cat ctt gtt tta ttg act ttg att tcc ttt aga   51
p0711              Met Val Ile Pro His Leu Val Leu Leu Thr Leu Ile Ser Phe Arg    15
                    $               $   $   $   $       $   $


GNSQ_0711          tta aaa gaa aaa aat agt gta ttt cat tta att ttc ccc gct att   96
p0711              Leu Lys Glu Lys Asn Ser Val Phe His Leu Ile Phe Pro Ala Ile    30


GNSQ_0711          cac agt tta tgc tta tgt gat tct gga aga att cca gct agg aat   141
p0711              His Ser Leu Cys Leu Cys Asp Ser Gly Arg Ile Pro Ala Arg Asn    45
                            $       $


GNSQ_0711          gcc ttg gac cca tcc cag gac cag caa ccc ctg cag cag gac aaa   186
p0711              Ala Leu Asp Pro Ser Gln Asp Gln Gln Pro Leu Gln Gln Asp Lys    60


GNSQ_0711          gat ggc act gag act atg tgt gta gct gga agc aac cta aat gtc   231
p0711              Asp Gly Thr Glu Thr Met Cys Val Ala Gly Ser Asn Leu Asn Val    75
                                        $


GNSQ_0711          cat tcg tgg gtg aat gaa gaa aga aaa tgt ggc ata tcc ata caa   276
p0711              His Ser Trp Val Asn Glu Glu Arg Lys Cys Gly Ile Ser Ile Gln    90
                                                    $


GNSQ_0711          tgt aat atc att cag cct tta caa agt agg aaa ctc tgc cgt ttg   321
p0711              Cys Asn Ile Ile Gln Pro Leu Gln Ser Arg Lys Leu Cys Arg Leu   105

                    reverse
GNSQ_0711          ctg caa cag aga tga                                           336
p0711              Leu Gln Gln Arg STOP                                          109
                    $
```

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Figure 3

```
GNSQ_2882   ggaagt atg agt cct agt tta ttc ttc att ttt aag att gtt ttg gct att   51
p2882              Met Ser Pro Ser Leu Phe Phe Ile Phe Lys Ile Val Leu Ala Ile   15
                    S                         S           S   S   S       S

GNSQ_2882          gtg gat tcc ctg caa ttc tat atg aat ttc gaa tca gtt tgt cga   96
p2882              Val Asp Ser Leu Gln Phe Tyr Met Asn Phe Glu Ser Val Cys Arg   30
                    S                                               S

GNSQ_2882          tgt ctg caa aaa atc tct gtg att ctg ata ggg att gct ttt aac  141
p2882              Cys Leu Gln Lys Ile Ser Val Ile Leu Ile Gly Ile Ala Phe Asn   45
                    S

GNSQ_2882          ctg tgt aac gat ttg ggg agt att gtc att tta aca gtg tta tgt  186
p2882              Leu Cys Asn Asp Leu Gly Ser Ile Val Ile Leu Thr Val Leu Cys   60
                                                                            S

GNSQ_2882          att cta atc cat gaa tat gaa ata tat ttc ctt ttg ttt aga tct  231
p2882              Ile Leu Ile His Glu Tyr Glu Ile Tyr Phe Leu Leu Phe Arg Ser   75

GNSQ_2882          ttg att ttt tca tta tgt ttt ata gtt cca gag tat agt aag ttt  276
p2882              Leu Ile Phe Ser Leu Cys Phe Ile Val Pro Glu Tyr Ser Lys Phe   90
                                        S

GNSQ_2882          tgc aat ttt tat gtt aaa ttt att ctt aag aat tta ttt ttg atg  321
p2882              Cys Asn Phe Tyr Val Lys Phe Ile Leu Lys Asn Leu Phe Leu Met  105

GNSQ_2882          cta tca taa                                                  330
p2882              Leu Ser STOP                                                 107
                            S
```

Figure 4

```
GNSQ_4711  tctagg atg gta act cct atc tgg aca ctt ttc att tgt tac tgt ttg acc   51
p4711             Met Val Thr Pro Ile Trp Thr Leu Phe Ile Cys Tyr Cys Leu Thr    15
                   S                                               S

GNSQ_4711         tct ttg ctt gta tta cag gct ata ttt aaa gaa ata gat aac att    96
p4711             Ser Leu Leu Val Leu Gln Ala Ile Phe Lys Glu Ile Asp Asn Ile    30
                   S   S   S   S

GNSQ_4711         ctc tct gag gtt gat tta aac caa cat cct gta cgt tgc tgc tat   141
p4711             Leu Ser Glu Val Asp Leu Asn Gln His Pro Val Arg Cys Cys Tyr    45
                                                               S   S

GNSQ_4711         agc ttc cca aca ttt tgt gta gag ggg atg cta ttg aag ttg tgt   186
p4711             Ser Phe Pro Thr Phe Cys Val Glu Gly Met Leu Leu Lys Leu Cys    60

GNSQ_4711         ttt aat atg gag cca cac tgt ttt ctt tct ctg acc cag tct aca   231
p4711             Phe Asn Met Glu Pro His Cys Phe Leu Ser Leu Thr Gln Ser Thr    75
                                           S

GNSQ_4711         gtc agc ctg tcc caa ggc tgc cat cta ttc tct gtg ttt gtg cag   276
p4711             Val Ser Leu Ser Gln Gly Cys His Leu Phe Ser Val Phe Val Gln    90
                                       S

GNSQ_4711         ctc atc tgg aca gct cat ctg gac aga cac aaa gaa tag          315
p4711             Leu Ile Trp Thr Ala His Leu Asp Arg His Lys Glu STOP         102
                                                                   S
```

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Figure 5

```
                          forward
GNSQ_4320  tgtaat atg tta ttt act tta tta ttc cga att cta atc ggt tat gtg aga   51
p4320             Met Leu Phe Thr Leu Leu Phe Arg Ile Leu Ile Gly Tyr Val Arg    15
                   S            S   S           S   S   S           S

GNSQ_4320         act ctg tgg acg aaa aat tct tgc tgc tgt tgg cga atg att tta   96
p4320             Thr Leu Trp Thr Lys Asn Ser Cys Cys Cys Trp Arg Met Ile Leu    30
                                              S   S

GNSQ_4320         aat cat tca ttt aaa caa gaa gtg cct atg att gta gag cta aag  141
p4320             Asn His Ser Phe Lys Gln Glu Val Pro Met Ile Val Glu Leu Lys    45

GNSQ_4320         caa aaa tgt gaa atg ttt tgt cag aaa tat cta gtt gat aaa gat  186
p4320             Gln Lys Cys Glu Met Phe Cys Gln Lys Tyr Leu Val Asp Lys Asp    60
                           S

GNSQ_4320         tat tcc ttt cgt gtt tct gta acc tgt cag ttc ttt ata ctt tta  231
p4320             Tyr Ser Phe Arg Val Ser Val Thr Cys Gln Phe Phe Ile Leu Leu    75
                                              S

GNSQ_4320         cat gat tcc tac cca act gag aat aca tgg tca act att cca aca  276
p4320             His Asp Ser Tyr Pro Thr Glu Asn Thr Trp Ser Thr Ile Pro Thr    90
                                        reverse
GNSQ_4320         ttg tct gct ctt ata tcc tct ttg att ttt ctg tga             312
p4320             Leu Ser Ala Leu Ile Ser Ser Leu Ile Phe Leu STOP            101
                                                                    S
```

Figure 6

```
                    _____forward_____►
GNSQ_5008  ccagac atg atc ttt ggc ctg cta atc aaa gct ctt tat cta gcg tca gcc   51
p5008             Met Ile Phe Gly Leu Leu Ile Lys Ala Leu Tyr Leu Ala Ser Ala   15
                   S              S   S   S           S


GNSQ_5008         tgg gca ggg gct ctg agc ctc ggc gct gct ggc att tgg ggc tgg   96
p5008             Trp Ala Gly Ala Leu Ser Leu Gly Ala Ala Gly Ile Trp Gly Trp   30


GNSQ_5008         atg act ctt tgc tgt ggc tgc tgt cct gtg cat tac agg aca tta  141
p5008             Met Thr Leu Cys Cys Gly Cys Cys Pro Val His Tyr Arg Thr Leu   45
                              S   S


GNSQ_5008         cgt agc atc cct gac cac aac cta cta gat gcc agt agc acc ccc  186
p5008             Arg Ser Ile Pro Asp His Asn Leu Leu Asp Ala Ser Ser Thr Pro   60


GNSQ_5008         tcc cta gtt atg aca acc aga aac atc tcc aga cat tgc caa tgt  231
p5008             Ser Leu Val Met Thr Thr Arg Asn Ile Ser Arg His Cys Gln Cys   75
                                                              S


GNSQ_5008         ccc ctg gtg gca aaa tca tcc ccg gct gag aat gag tgt tgc acg  276
p5008            ·Pro Leu Val Ala Lys Ser Ser Pro Ala Glu Asn Glu Cys Cys Thr   90
                                                                  S


GNSQ_5008         gta att cct cca ttc caa att aac aga gca ctt agg aac gag tgc  321
p5008             Val Ile Pro Pro Phe Gln Ile Asn Arg Ala Leu Arg Asn Glu Cys  105

                     ◄_____reverse_____
GNSQ_5008         ttt ctc cta tta ctt tcc ctt taa                           345
p5008             Phe Leu Leu Leu Leu Ser Leu STOP                          112
                                           S
```

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Figure 7

```
                              forward
GNSQ_0210  tgaact atg ggc ttt gtt gtt cta tgc cta att ttc ttc ctg tgt aag act   51
p0210            Met Gly Phe Val Val Leu Cys Leu Ile Phe Phe Leu Cys Lys Thr   15
                  S               S   S           S   S           S

GNSQ_0210         gga atg gat tcc aga ttt caa cta aaa ctc ttg ttt cac tgt ttt   96
p0210             Gly Met Asp Ser Arg Phe Gln Leu Lys Leu Leu Phe His Cys Phe   30

GNSQ_0210         caa gga ctt ttc caa agg tca cac atg gac tat tgt gat gaa tgc   141
p0210             Gln Gly Leu Phe Gln Arg Ser His Met Asp Tyr Cys Asp Glu Cys   45
                                                          S           S

GNSQ_0210         act ctg cag ggt gtg ttc cca gag cac aga agt aac cag aga gct   186
p0210             Thr Leu Gln Gly Val Phe Pro Glu His Arg Ser Asn Gln Arg Ala   60

GNSQ_0210         gca agg gag gtg ttg ccc aca cca aaa cac tgc aga ctt att ccc   231
p0210             Ala Arg Glu Val Leu Pro Thr Pro Lys His Cys Arg Leu Ile Pro   75
                                                          S

GNSQ_0210         ctg ggg aca gtg ctg tca gag tgt cca ttt caa gct ccc tgt tgg   276
p0210             Leu Gly Thr Val Leu Ser Glu Cys Pro Phe Gln Ala Pro Cys Trp   90
                                                                      S

GNSQ_0210         cca cag aca aaa gcc att atc cta aat ctc tgg cga aac ttg gag   321
p0210             Pro Gln Thr Lys Ala Ile Ile Leu Asn Leu Trp Arg Asn Leu Glu   105

GNSQ_0210         gtc tta gaa gtg gac aga agt tta aga cag gat tgc ttt aaa tgc   366
p0210             Val Leu Glu Val Asp Arg Ser Leu Arg Gln Asp Cys Phe Lys Cys   120

                         reverse
GNSQ_0210         aca att ttg tta gaa ttt ttc tga                            390
p0210             Thr Ile Leu Leu Glu Phe Phe STOP                          127
                                              S
```

Figure 8

```
                       forward
GNSQ_4922  ctgact atg atg agg gtg cta agg ctg ctg gcg agg gtc ctc ctc ggc cag   51
p4922             Met Met Arg Val Leu Arg Leu Leu Ala Arg Val Leu Leu Gly Gln    15
                   S               S       S   S           S   S   S

GNSQ_4922         ctt ctc cta gca gca ggg cac gca cag ccc tgt ttt ctc atc tgc   96
p4922             Leu Leu Leu Ala Ala Gly His Ala Gln Pro Cys Phe Leu Ile Cys    30
                                                       S                   S

GNSQ_4922         ttt cag cag cat ttg cct cct act cca ctt ggg tca ctc aag ggt  141
p4922             Phe Gln Gln His Leu Pro Pro Thr Pro Leu Gly Ser Leu Lys Gly    45

GNSQ_4922         ccc aaa ata gac ctg tgc att cat ggg acc cct ccc acc tgc ctc  186
p4922             Pro Lys Ile Asp Leu Cys Ile His Gly Thr Pro Pro Thr Cys Leu    60
                                       S

GNSQ_4922         tct gct cag tgt ctc tgt tgg gac agg cag caa gtg ctt aaa tcc  231
p4922             Ser Ala Gln Cys Leu Cys Trp Asp Arg Gln Gln Val Leu Lys Ser    75
                                       S                            reverse
GNSQ_4922         cag cca ctg ctc ccc gct gga gtc cac ctg aga act ttc cca gca  276
p4922             Gln Pro Leu Leu Pro Ala Gly Val His Leu Arg Thr Phe Pro Ala    90

GNSQ_4922         att tga                                                       282
p4922             Ile STOP                                                       91
                       S
```

Figure 9

<u>N-Terminal Region</u>

```
CXCL1      MARAALS --AAPSNPR---LLRVALLLLLLVAAGRRAAG
CXCL2      MARATLS --AAPSNPR---LLRVALLLLLLVAASRRAAG
CXCL3      MAHATLS --AAPSNPR---LLRVALLLLLLVGSRRAAGAS
CXCL4      MS --SAF--CASRPG----LLFLGLLLLPLVVAFASA
CXCL5      MSLLSSR --AARVPGPSSSLCALLVLLLLLTQPGPIASA
CXCL6      MSLPSSR --AARVPGPSGSLCALLALLLLLTPPGPLASA
CXCL7      MSLRLDTTPSCNSARPLHALQVLLLLSLLLTALASSTKGQTKRNLAKGKEE
CXCL8      MT ---SKL-A---------V-ALLAAFLI-SAALCEG
CXCL9      MKKSG -------------VLFLLGIILLVLIGVQG
CXCL10     MNQTA --------------I-LICCLIFLTLSGIQG
CXCL11     MSVKGM ------------AIALAVILCATVVQG
p1754      MNVI --------------VLQFILLVFLLVKIYKHADTLFYI
p0711      MVIPH --------------LV-LLTLISFRLKEKNSVFH
p2882      MSPS --------------L-FFIFKIVLAIVDSL
p0210      MGFVVLCLIFFLCKTGMDSRFQLKLLFHCFQGL
p4922      MMR ----------------VLRLLARVLLGQLLLAA
```

<u>Cys-rich region</u>

```
CXCL1      ASVATELRCQ --CLQTLQGIHPKN-IQSVNVKSPG------PHCAQTE--VIATLKNGRKA---C
CXCL2      APLATELRCQ --CLQTLQGIHLKN-IQSVKVKSPG------PHCAQTE--VIATLKNGQKA---C
CXCL3      VVTELRCQ --CLQTLQGIHLKN-IQSVNVRSPG------PHCAQTE--VIATLKNGKKA---C
CXCL4      EAEEDGDLQCL --CVKTTSQVRPRH-ITSLEVIKAG------PHCPTAQ--LIATLKNGRK---IC
CXCL5      GPAAAVLRELRCV --CLQTTQGVHPKM-ISNLQVFAIG------PQCSKVE--VVASLKNGKE---IC
CXCL6      GPVSAVLTELRCT --CLRVTLRVNPKT-IGKLQVFPAG------PQCSKVE--VVASLKNGKQ---VC
CXCL7      SLDSDLYAELRCM --CIKTTSGIHPKN-IQSLEVIGKG------THCNQVE--VIATLKDGRK---IC
CXCL8      AVLPRSAKELRCQ --CIKTYSKPFHPKFIKELRVIESG------PHCANTE--IIVKLSDGRE---LC
CXCL9      TPVVRKGRCS --CISTNQGTIHLQSLKDLKQFAPS------PSCEKIE--IIATLKNGVQT---C
CXCL10     VPLSRTVRCT --CISISNQPVNPRSLEKLEIIPAS------QFCPRVE--IIATMKKKGEKR--C
CXCL11     FPMFKRGRCL --CIGPGVKAVKVADIEKASIMYPS------NNCDKIE--VIITLKENKGQR--C
p1754      YIPIYVCM --CIH-SYALYNSILVSDGLRMLR---------CSHK----IIISTLTITF---LC
p0711      LIFPAIHSLCL --CDSGRIPARNALDPSQDQQPLQQDKDGTETMCVAGSNLNVHSWVNEERK---C
p2882      QFYMNFESVCR --CLQKISVIL-IGIAFNLCNDLGS IVILTV-LCILIHEYEIYFLLFRSLIFSLC
p0210      FQRSHMDYCDE -CTLQGVFPEHRSNQRAAREVLPTP-----KHCRLIPLGTVLSECPFQAP---C
p4922      GHAQPCFLICFQQHLPPTPLGSLKGPKID----------LCIHGTPPTCLSAQC------LC
                   §      §                               §                        §
```

<u>C-terminal region</u>

```
CXCL1                    LNPASPIVKKIIEKMLNSDKSN
CXCL2                    LNPASPMVKKIIEKMLKNGKSN
CXCL3                    LNPASPMVQKIIEKILNKGSTN
CXCL4                    LDLQAPLYKKIIKKLLES
CXCL5                    LDPEAPFLKKVIQKILDGGNKEN
CXCL6                    LDPEAPFLKKVIQKILDSGNKKN
CXCL7                    LDPDAPRIKKIVQKKLAGDESAD
CXCL8                    LDPKENWVQRVVEKFLKRAENS
CXCL9                    LNPDSADVKELIKKWEKQVSQKKKQKNGKKHQKKKVLKVRKSQRSRQKKTT
CXCL10                   LNPESKAIKNLLKAVSKERSK RSP
CXCL11                   LNPKSKQARLIIKKVERKNF
p1754                    LHAEILTNGLQLPTVFSTPACCTGW
p0711                    GISIQCNIIQPLQSRKLCRLLQQR
p2882                    FIVPEYSKFCNFYVKFILKNLFLMLS
p0210          WPQTKAIILNLWRNLEVLEVDRSLRQDCFKCTILLEFF
p4922              WDRQQVLKSQPLLPAGVHLRTFPAI
```
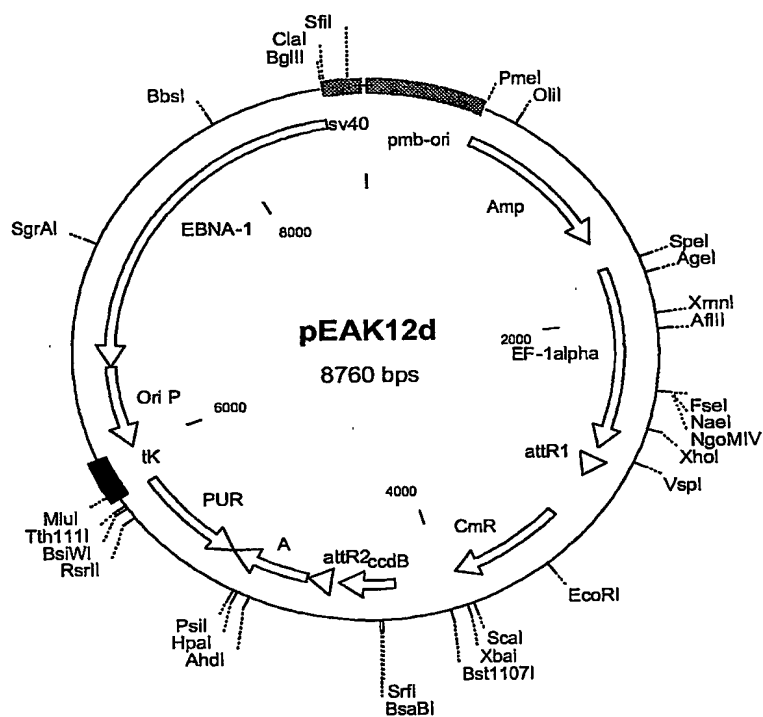
Figure 10

<u>N- Terminal Region</u>

```
CCL1    MQIITTALVCLLLAGMWPEDVD SKSMQV
CCL2    MKVSAALLCLLLIAATFIPQGLAQPDAIN
CCL3    MQVSTAALAVLLCTMALCNQFSASLAAD
CCL4    MKLCVTVLSLLMLVAAFCSPALSAPMGSD
CCL5    MKVSAA ALAVILIATALCAPASASPYSS
CCL7    MKASAALLCLLLTAAAFSPQGLAQPVGIN
CCL8    MKVSAALLCLLLMAATFSPQGLAQPDSVS
p4711   MVTPIWTLFICYCLTSLLVLQAIFKEIDNILSEVDLNQ
p4320   MLFTLLFRILIGYVRTLW
p5008   MIFGLLIKALYLASAWAGALSLGAAGIWG
```

<u>Cys-rich region</u>

```
CCL1    PFSRCCFSFAEQEIPLRAILCYRN -TSSI-------------CSNEGLIFKLKRGKEA -CALD
CCL2    APVTCCYNFTNRKISVQRLASYRRITSSK -------------CPKEAVIFKTIVAKEI -CAD
CCL3    TPTACCFSYTSRQIPQNFIADYFE -TSSQ-------------CSKPGVIFLTKRSRQV -CAD
CCL4    PPTACCFSYTARKLPRNFVVDYYE -TSSL-------------CSQPAVVFQTKRSKQV -CAD
CCL5    DTTPCCFAYIARPLPRAHIKEYFY -TSGK-------------CSNPAVVFVTRKNRQV -CAN
CCL7    TSTTCCYRFINKKIPKQRLESYRRTTSSH -------------CPREAVIFKTKLDKEI -CAD
CCL8    IPITCCFNVINRKIPIQRLESYTRITNIQ -------------CPKEAVIFKTKRGKEV -CAD
p4711   HPVRCCYSFPTFCVEGMLLKLCFNMEPH ------------ ----CFLSLTQSTVSLSQG --CHL
p4320   TKNSCCCWRMILNHSFKQEVPMIVELKQK ---------- CEMFCQKYLVDKDYSFRVSVTCQFF
p5008   WMTLCCGCCPVHYRTLRSIPDHNLLDASSTPSLVMTTRNISRHCQCPLVAKSSPAENE  --CCTV
                 $$                                  $            $
```

<u>C-terminal region</u>

```
CCL1            TVGWVQRHRKMLRHCPSKRK
CCL2            PKQKWVQDSMDHLDKQTQTPKT
CCL3            PSEEWVQKYVSDLELSA
CCL4            PSESWVQEYVYDLELN
CCL5            PEKKWVREYINSLEMS
CCL7            PTQKWVQDFMKHLDKKTQTPKL
CCL8            PKERWVRDSMKHLDQIFQNLKP
p4711           FSVFVQLIWTAHLDRHKE
p4320   ILLHDSYPTENTWSTIPTLSALISSLIFL
p5008           IPPFQINRALRNECFLLLLSL
```

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Figure 11